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Maximum Match 100%
Listing first 45 summaries
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     on:
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   648.5
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1641
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Copyright (c) 1993 - 2000 Comp
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WABB_ECOLI
NODL_RHITU
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THGA_ECOLI
YJVB_YEAST
YA39_SCHPO
NODL_RHIME
LPXD_RICRI
MAA_BACSU
LPXD_RICRI
MAA_ECOLI
LPXA_AGUAE
TABB_PSESZ
CAPG_STAAU
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962.095 Million cell updates/sec
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P51002
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P29847 salmonella
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6 rhizobium m
3 rickettsia
5 bacillus su
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SUBUNIT. MEDLINE-200850 Hindson V.J., "Serine acetyl trimers."; J. Biol. Chem! CATALYTIC SERINE! ENZYME REG -!- SATHWAY: C -!- SUBUNIT: H	STRAIN-KI 2/ STRAIN-KI 2/ STRAIN-KI 2/ SOFIA H.J., "Analysis of region from Nucleic Acid (4) (4) (4) (CHARACTERIZA MEDLINE-9109) Wigley D.B., "The serine purification FEBS Lett. 2 [5]	SEQUENCE FROM N.A. STRAIN-K12; MEDLINE-90211342; Tei H., Murata K., Tei H., Murata K., Tei H., Murata K., Structure and extended to the structure oli K-12 cyse loo Biochem. Biophys.	ENC D. D. yst ess an en.	7 B B B B .	1 SE_ECOLI 5796; -NOV-198! -NOV-1988 -MAY-2000		112.5 112 112 1112 1106.5 106.5 104.5 103.5 103.5
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PubMed=10617639; dy P.C., Rowe A.J., Shaw W nsferase from Escherichia 5:461-466(2000). IVITY: ACETYL-COA + L-SERI TION: SENSITIVE TO FEEDBAC EIME BIOSYNTHESIS. HEXAMER. DIMER OF A HOMOTR	pubmed=8041620; pubmed=8041620; Daniels D.L., plunk Scherichia coli genome. V co 81.5 minutes."; co 81.5 minutes."; co 81.5 minutes."; pubmed=2125278; ck J.P., Shaw W.V.; transferase from Escheric reliminary crystallograph	08679; .; f cysx, the sec un. 167:948-955	ubMed=3309158; hesis in Escherichia col erine acetyltransferase -excreting mutant."; 133:515-525(1987).	teria; gamma subdivision	NDARD; PRT; 273 AA 19, Created) 19, Last sequence update) 19, Last annotation updat 19, East annotation updat	,	456 1 GCAD_BACSU 116 1 GCAD_BACCL 456 1 GLMU_ECOLI 209 1 SATA_ENTEC 456 1 GLMU_HAEIN 1456 1 GLMU_HAEIN 1456 1 GLMU_HAEIN 1456 1 GLMU_HAEIN 1456 1 DAPD_HUCAP 171 1 DAPD_BUCAP 171 1 DAPD_HUCAP 171 1 DAPD_HUCAP 171 1 CAT4_AGRTU 170 1 CAT4_AGRTU 171 1 CAT4_AGRTU 171 1 CAT4_BCOLI
COli is a dimer of NE = COA + O-ACETYL-L- K INHIBITION BY L-CYSTEINE.	ett G. III, Blattner F.R.; . DNA sequence of the . hia coli. Over-expression, ic analysis.";	ond gene in the Escherichia	.i: nucleotide sequence and (cysE) gene from the wild-	; Enterobacteriaceae;	∵ <u>°</u>	. AAAAA MAFAMICEFRA	P14192 bacillus su P42817 bacillus ca P17114 escherichia P50870 enterococcu P43889 haemophilus P18482 salmonella P43888 haemophilus P43284 haemophilus P45284 haemophilus P528638 escherichia

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Matches 132
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PIR; A34563; A34563.
ECOZDBASE; H029.3; 6TH EDITION
ECOGENE; EGIOL87; cysE.
InterPro; IPRO01451; -.
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                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
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                                                                                                                                                                                                                                                                                                   SALTY
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Pfam; PF00132; hexapep_TRANSFERASES; 1.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
SEQUENCE 273 AA; 29316 MW; 466EB898750EF709 CRC64;
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Rogers G.E.;
                                                                                                                                                                                                                                                                      P29847;
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                 SEQUENCE FROM N.A.
                                             Submitted (MAY-1991)
                                                            Sivaprasad A.V.,
                                                                               STRAIN=LT2;
                                                                                            SEQUENCE FROM N.A.
                                                                                                                          NCBI_TaxID=602;
                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                       Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103
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SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQ 162
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                                                                                                                                                                                                                                                                                   SALTY
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                                                                                                                                                                                                                                                                                                                                                                                                                        GTGKSGGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRRALAIFLQNQVSVTFQVDIHPAAKIGRGIMLDHATGIVVGETAVIENDVSILQSVTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG 222
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                                                                                                                                                                                                                                                                                   STANDARD;
                                                            Kuczek E.S.,
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                                             ., Bawden C.S., Roy
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 648.5; DB 1; Pred. No. 3.1e-44;
                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                          subdivision;
                                                                                                                                                                                                                                                                                   273 AA.
                                                             Rogers G.E.;
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                                                                                                                                                          Enterobacteriaceae,
                                                databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- ENZYME REGULATION: SENSITIVE TO FEEDBACK INHIBITION BY L-CYSTEINE !- PATHWAY: CYSTEINE BIOSYNTHESIS.
-!- SUBUNIT: HOMOHEXAMER. DIMER OF A HOMOTRIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent number GB2227243, 25-JUL-1990.
-!- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPED_TRANSFERASES; 1.

Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.

SEQUENCE 273 AA; 29291 MW; 6A5736E656FED25B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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SEQUENCE FROM N.A.
STRAIN=RD / KW20 / ATCC 51907;
STRAIN=S5550630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White
                                                                                                                                           Haemophilus influenzae
                                                                                                                                                                                                                    01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                      CYSE_HAEIN P43886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; A00198; CAA00039.1
PIR; S29568; S29568.
StyGene; SG10073; cysE.
InterPro; IPR001451; -.
                                                                                          NCBI_TaxID=727;
                                                                                                         Haemophilus
                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                  CYSE OR HI0606
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGKTSGDRHPKIREGVMIGAGAKILGNIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRRALAIFLQNQVSVSFQVDIHPAAKIGRGIMLDHATGIVVGETAVIEDDVSILQSVTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLG
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51.2%;
                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                              gamma
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Pred. No. 3.1
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                                                                                                                              subdivision;
   o
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                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                  update)
   Clayton
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                                                                                                                                Pasteurellaceae;
     R.A.,
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   E.F.,
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2

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RESULT 4
CYSE_BU CYSE_B
AC P57162
DT 01-OCT
DT 01-OCT
DT SERINE
GN CYSE 0
GN CYSE 0
OS Buchne
OS Symbio
OC Bacter
OX NCBL_T
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Best Local S
Matches 125
                                                                                        CYSE_BUCAI STANDARD; PRT; 274 AA. P57162; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                   symbiotic bacterium).
Bacteria; Proteobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   Bacteria; Proteobacteria; gamma subdivision; Buchnera NCBI_TaxID=118099;
                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon
                                                                            CYSE OR BU054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00132; hexapep; 2.

PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.

Transferase; Acyltransferase; Cysteine biosynthesis;
SEQUENCE 267 AA; 29166 MW; 93428DE9D504DFB4 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            VALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELF 106
                                                                                                                                                                                                                                                                                        ----SQDKAAKPAFDMNQ 254
                                                                                                                                                                                                                                                                                                                           ENPRKHDKI - - PCLTMDQ
                                                                                                                                                                                                                                                                                                                                                               ESGDRHPKVREGYMIGAGAKILGNIEVGKYAKIGANSVVLNPVPEYATAAGVPARIV---
                                                                                                                                                                                                                                                                                                                                                                                                                                      LALYLQNQISVAFDVDIHPAAKIGHGIMFDHATGIVVGETSVIENDVSILQGVTLGGTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEAYQSNPSIIDCAACDIQAVRHRDPAVELWSTPLLYLKGFHAIQSYRITHYLWNQNRKS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVWQHIRQEAKELAENEPMLASFFHSTILKHQNLGGALSYLLANKLANPIMPAISLREII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 624.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 5
CYSE_BUCAP
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 116;
                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishika "Genome sequence of the endocellular bacterial symbiont Buchnera sp. APS.";
Nature 407:81-86(2000).

-!- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-
                                               Gene
                                                                          endosymbiont of aphids) containing
                                                                                      "Sequence analysis of a DNA fragment
                                                                                                                                                                                                          Buchnera aphidicola (subsp.
                                                                                                                                                                                                                                                                                                          P32003;
                                                                                                                                                                                                                                                                                                                      CYSE_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; F
SEQUENCE 274 AA; 30165 MW; 553D252F1048B6B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93012960; PubMed=1398077;
                                                                                                                                                                            NCBI_TaxID=98794;
                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP001118; BAB12777.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-TOKYO 1998;
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                                                                                                                                                                                                                                                                                                                                                                                                          189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                         E, and secb.";
e 119:113-118(1992).
CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE =
PATHWAY: CYSTEINE BIOSYNTHESIS
                SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLYLQSRISSEFSVDIHPAAFIGSGVMLDHATGIVIGEGVTIENDVSILHSVTLGGTGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVYLNDRSILNFIVQDIKAVLKRDPAVNDYLTPLLYLKGFHALEAYRISHYLWNTGKKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IWNKILYDVSFLLKKEPILSDFYQSSILQHQSFTSSLSYILSNKLSTSMISEKKIQGIFD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                     -SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                           Proteobacteria;
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                                                                                                                                                                                                      Schizaphis graminum)
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Pred. No. 2.6e-38;
"" matches 73;
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                                                                          genes
                                                                                            from
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                                                                          homologous
                                                                                           Buchnera
                                                                                                                                                                                            Buchnera
                              COA +
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                            O-ACETYL-L-
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CYSE_SYNP7
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Best Local
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                                                                                                                              SEQUENCE FROM N.A.

MEDILINE-96281517; PubMed-8661945;

Anandan S., Nalty M.S., Cogdell D.E., Golden S.S.;

"Identification of two classes of transcriptional recthe cyanobacterium Synechococcus sp. strain PCC 7942.

Arch. Microbiol. 166:58-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
This
                                                                                                                                                                                                                                                                 CYSE.
Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                Q56002;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001451; -.
Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  SERINE ACETYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
                                                                                                                                                                                                                                                NCBI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                 CYSE_SYNP7
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                           SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF (LIV)-G-X(4).
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                                                                                                                  CATALYTIC ACTIVITY:
                                                                                 PATHWAY: CYSTEINE BIOSYNTHESIS.
                                                                                                SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JC1293; JC1293.
SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGK 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTGKNRHPIIRKNVTIGAGAKILGNIEVGQGVKVGAGSIVLKNIPPFVTVVGVPAKIIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSAYLQSRISTVFSVDIHPAASIGSGIMLDHATGIVIGEGVIIENDVSIFHSVTLGGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKIYANNISIINSVVKDIKAASQRDPVVKHYLTPLLYLKGFHALEAYRLSHYLWNIKRYE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELWNMIKHKAQKILKKEPILSNFYQKSILNHKKLSHSLSCILSDKLSTSMISEKDIYNIF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 ĀA;
                                                                                                                                                                                                                                                                                                              (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
YLTRANSFERASE (EC 2.3.1.30) (SAT).
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61 AA; 28914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.5%;
                                                                                                                  ACETYL-COA + L-SERINE = COA +
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                   244 AA
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                                                                                                                                                                  regulator
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Best Local (
                                                                                                                                                                                     Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the subtilis chromosome containing the replication origin."; DNA Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYSE OR CYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           006750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Transferase; Acyltransferase; Cysteine biosynthesis; F
SEQUENCE 244 AA; 26453 MW; AB0B50491023EDB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                             "Clustering and co-transcription of the Bacillus subtilis genes encoding the aminoacy1-tRNA synthetases specific for glutamate and for cysteine and the first enzyme for cysteine biosynthesis."; J. Biol. Chem. 269:7473-7482(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYSE_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L41665; AAB38543.1; -.
                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                     Gagnon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                              MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94171772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 AGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI---GGKENPRKHDKIP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 IHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                        CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE =
                                                                                                                                        PATHWAY: CYSTEINE BIOSYNTHESIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7510287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group;
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Pred. No. 4.4e-27
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Best Local
                                                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajina N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                   CYSE_SYNY3 STANDARD; PRT; 249 AA P74089; Q55209; Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT.
                                                                                                                                                                                                                                                              Sakamoto T., Wada H., Nishida I., Ohta H., Murata N.;
"Sequence analysis of a DNA fragment from Synechocystis PCC6803 containing genes homologous to cysE (serine acetyltransferase) (glucose-6-phosphate isomerase).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _SYNY3
                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. Bacteria; Cyanoba
                                                                                                                                                                                                                                                                                                                                                                                                             CYSE OR SLR1348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01246; 1BST.
SubtiList; BG10155; cysE.
InterPro; IPR001451; -.
                                                                                                                                                                                                   MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Acyltransferase; SEQUENCE 217 AA; 24143 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L14580; AAA21797.1; -.
EMBL; D26185; BAA05327.1; -.
EMBL; Z99104; CAB11869.1; -.
EMBL; B53402; B53402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Plant Mol.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1148;
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PROSITE; PS00101; HEXAPEP_TRANSFERASES;
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    SUBCELLULAR LOCATION:
              PATHWAY: CYSTEINE BIOSYNTHESIS
                                               CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                           Cyanobacteria; Chroococcales; Synechocystis
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                                             ACETYL-COA + L-SERINE =
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                                                                                                                                                                                                                                                                              acetyltransferase) and pgi
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                                             COA + O-ACETYL-L-
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Best Local
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01-NOV-1997
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                     xylosus."
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=DSM 20267 / C2A;
MEDLINE=97237691; PubMed=9084146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus xylosus.
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SEQUENCE 249 AA; 27336 MW; ED5EC58D659DCFBB CRC64;
                                                                                                                                                                                                                                                                                       FEMS Microbiol.
                                                                                                                                                                                                                                                                                                                                                                          Fiegler H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYSE_STAXY
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PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
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                                                                                SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                 PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                            CATALYTIC
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                                                                                                                                                                                                                                                                                                                                       cation of the serine acetyltransferase gene of Staphylococcus
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7 (Rel. 35,
8 (Rel. 37,
                                                                                                                                                                                                                                                                                                                                                                       Brueckner R.
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                                                                                                                                                                                                                                                            ACTIVITY: ACETYL-COA
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                                                                                                                                                                                                                                                                                       Lett. 148:181-187(1997)
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                                                                                                                                                                                                                                                                                                                                                                                  Evans D.J., Jones R., Woodley P.R., Wilborn J.R., Robson R.L.;

"Nucleotide sequence and genetic analysis of the Azotobacter chrococccum nifuswaxm gene cluster, including a new gene (nifp) encodes a serine acetyltransferase.";

J. Bacteriol. 173:5457-5469(1991).

-i- FUNCTION: PROBABLE SERINE ACETYLTRANSFERASE REQUIRED FOR OPTIMIZING THE EXPRESSION OF NITROGENASE ACTIVITY. NIFP MAY REQUIRED TO BOOST RATES OF SYNTHESIS OR INTRACELLULAR CONCENTRATIONS OF CYSTEINE OR METHIONINE.

-i- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOY-1991 (Rel. 20, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
PROBABLE SERINE ACETYLTRANSFERASE (EC 2.3.1
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01-NOV-1991 (Rel.
01-JUN-1994 (Rel.
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Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
SEQUENCE 216 AA; 24000 MW; 728FE804A0D7282C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001451; -.
Pfam; PF00132; hexapep; 2.
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EMBL; M60090;
                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=91358323;
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                                                                                                                                                                              European Bioinformatics Institute.
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                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration
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Pred. No. 1.1e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
2.3.1.30)
                                                                                                                   There are no restrictions on it ing as its content is in "" ved. Usage by the end of the
                                                                                                                                                                                                                                                                                          REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SAT).
                                                                                                                                                                                                                                                                                                                                                                                              COA + O-ACETYL-L-
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
Nitrogen fixation; Transferase; Acyltransferase;
Cysteine biosynthesis.
SEQUENCE 269 AA; 28578 MW.
                                                                                                                                                                                  MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Fleson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
COtton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                           Peek R.M., Thompson S.A., Atherton J.C., Blaser M.J., Miller "Expression of a novel ulcer-associated gene, iceA, by H. pylfollowing contact with gastric epithelium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori (Campylobacter pylori). Bacteria; Proteobacteria; epsilon subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYSE OR HP1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YATEH,
                                                                                                                  Pyrori.";
Nature 388:539-547(1997)
                                                                                                                                                                   Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSE_HELPY
                                                                                                                                                     "The complete genome sequence of the
                                                                                                                                                                                                                                                                                                                                               STRAIN=26695
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                  -!- CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 IIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQN------RKIVAL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 KENP----RKHDKIP 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 DRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI----GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LVSN------VDIHPGAVIGARFFIDHGACVVIGETAEIGRDVTLYHGVTLGGTTGAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LLAQWREDIRCVFERDPAARTTFEVLTTYPGVHAIMLYRLAHRLWRPNALPRPAAVVRAR 62
                              PATHWAY: CYSTEINE BIOSYNTHESIS.
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE CYSE/LACA/LDXA/NODL FAMILY OF
                ACETYLTRANSFERASES. COMPOSED OF
                                                                                   SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLNPYGIDLDHHLIP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRHPTLGDVVLVGAGAKILGPITIGANARVGANSVVVQDVPEGCTVVGIPGKVVKLREAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                               (SEP-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                           49503 / 60190;
Thompson S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                               / ATCC 700392;
                                                                                                  ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.6%;
                                                                                                   ACETYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 369.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                   + L-SERINE = COA +
                MULTIPLE
                                                                                                                                                   gastric pathogen Helicobacter
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                REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat;
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                                                                                                       O-ACETYL-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
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CYSE_HELPJ
ID CYSE_HA
AC Q92KH14
AC Q92KH14
DT 01-OCT
CYSE O
OC Helico
OC Helico
OC NCENT
RA SEQUEN
RX MEDLIN
RA Alm R.
RA Tunmin
RA Tunmin
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Best Local
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 39:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ZK14;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99120557; PubMed=9923682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYSE OR JHP1133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYSE_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Acyltransferase; Cysteine biosynthesis; Repeat.
VARIANT 5 5 S -> F (IN STRAIN 60190).
VARIANT 110 110 K -> R (IN STRAIN 60190).
VARIANT 162 162 S -> T (IN STRAIN 60190).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 VLGAICVGDDVKIGANAVVLSDLPTGSTAVGSKAKTI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 VKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI 283
European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY) OF SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
                                                                                                                                                                                                                                                      PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY:
                                                                                                                                                  ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLQEDPAARNKWEVLLLYPGIHALLCYRLAHALHKRREYFIARALSQLARFITGIEIHPG
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TE; PS00101; HEXAPEP_TRANSFERASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Last sequence update) (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.2%; Score 365; DB 1; 45.2%; Pred. No. 4.1e-22;
                                                                                                                                                                                                                                                                                                              ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vovis G.F.,
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RESULT 13
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   Transferase; Ac
SEQUENCE 319
                                               Pfom; PF00132; hexapep; 2.
PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a cyanobacterial plasmid.";
Mol. Gen. Genet. 247:623-632(1995).
-!- CATALYTIC ACTIVITY: ACETYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last ann
SERINE ACETYLTRANSFERASE, PLAS
                                                                                                                                                EMBL; U23436; AAA86726.1; -.
                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholson M.L., Gaasenbeek M., Laudenbach "Two enzymes together capable of cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95327059; PubMed=7603442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pant.
Bacteria; Cya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechococcus sp. (strain PCC 7942) (Anacystis nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q59967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001541; AAD06715.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 VKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLIQNRVSESFAVDIHPG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 ILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLI 283
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                                                                                                                                                                                                                                                                                                                                                                                                        PATHMAI: CISTELL CONTROL OF SUBCELLULAR LOCATION: CYTOPLASMIC.

SUBLELULAR LOCATION: CYTOPLASMIC.

SIMILARITY: BELONGS TO THE CYSE/LACA/LDXA/NODL FAMILY OF ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: CYSTEINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQSGDRHPKIGDGVLIGAGSC 246
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                                                                                                                       IPR001451;
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Acyltransferase;
19 AA; 34570 MW;
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Last annotation update)
ASE, PLASMID (EC 2.3.1.30) (SAT).
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Pred. No. 1.2e-21;
Cysteine biosynthesis; Repeat;
00BB74D8AABB1E70 CRC64;
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2872B7539C3AC14A CRC64;
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P77558;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECOLI
                                                              Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshina T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., akono K., Wada C., Yamamoto Y., Horiuchi T., was also baka sequence of the Escherichia coli K.12 genome corresponding to the 40.1-50.0 min region on the linkaye map. DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.; "Organization of the Escherichia coli K-12 gene cluster responsible for production of the extracellular polysaccharide colanic acid."; Bacteriol. 178:4885-4893(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96326333; PubMed-8759852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
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                                                                                                                                                                                                                   MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 KGQARHPVIEDDVVIYAGATLLGRITVGRGSTIGGNVWLTRSVPA 299
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                                 PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME POLYSACCHARIDE COLANIC ACID.
                 SIMILARITY:
 ACETYLTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPA
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                                                                                                                                                                                                                                                                                                                       Shao Y.;
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                   BELONGS
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BIOSYNTHESIS ACETYLTRANSFERASE WCAB
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TO THE CYSE/LACA/LPXA/NODL COMPOSED OF MULTIPLE REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
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     REPEATS
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   OF [LIV]-G-X(4)
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PROSTTE; PS00101; HEXAPEP_TRANSFERASES; 1.
Lipopolysaccharide biosynthesis; Transferase; Acyltransferase;
SEQUENCE 162 AA; 17615 MW; F2462F836F3FB3AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U38473; AAC77837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
NODULATION PROTEIN L (EC 2.3.1.-).
                                                                                                                                                                                                            Canter Cremers H.C.J., Spaink H.P., Wijfjes A.H.M., Wijffelman C.A., Okker R.J.H., Lugtenberg B.J.J.; "Additional nodulation genes on the Sym plasmid of Fleguminosarum biovar victae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        Surin B.P., Downie J.A.; "Characterization of the Rhizobium leguminosarum involved in efficient host-specific nodulation."; Mol. Microbiol. 2:173-183(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid sym pRLIJI.

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium leguminosarum (biovar viciae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P08632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88246045; PubMed=3132583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
                                                                                                                                                                                                                                                                                                                                              MEDLINE=92003664; PubMed=2562395;
                                                             Downie J.A.;
                                                                                       MEDLINE=90136094; PubMed=2615659;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                              SIMILARITY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 SVVVKDVPARTTAVGNPARL 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVVLDSVPDNALVVGEKARV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INKNVVAGDDFTIRHGVTIGNRGADN-MACPHIGNGVELGANVIILGDITLGNNVTVGAG
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                             nodL gene from Rhizobium leguminosarum is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE000295; AAC75119.1; -. D90843; BAA15911.1; -.
      transferases encoded
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                                                                                                                                                                                     Biol. 13:163-174(1989)
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                                                                                                                           OTHER MEMBER OF THE CYSE/LACA/NODL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%;
37.1%;
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Pred. No. 1.8e-10;
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                                                                                                                                                                                                                                                   Sym plasmid of Rhizobium
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   cysE.";
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RL MOL. MICTODIOL. 3:1649-1651(1989).
CC -1- FUNCTION: ACETYLIPANSFERASE IMPLICATED IN THE O-ACETYLATION OF SINILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF ACETYLIPANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
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